



SEQUENCE LISTING

MCKEON, FRANK
YANG, ANNIE
LODA, MASSIMO
SIGNORETTI, SABINA
CRUM, CHRISTOPHER

<120> CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
RELATED THERETO

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Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	
145					150					155					160	
gag	gga	cag	att	gcc	cct	cct	agt	cat	ttg	att	cga	gta	gag	ggg	aac	528
Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	
				165					170					175		
agc	cat	gcc	cag	tat	gta	gaa	gat	ccc	atc	aca	gga	aga	cag	agt	gtg	576
Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	
			180					185					190			
ctg	gta	cct	tat	gag	cca	ccc	cag	gtt	ggc	act	gaa	ttc	acg	aca	gtc	624
Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	
		195					200					205				
ttg	tac	aat	ttc	atg	tgt	aac	agc	agt	tgt	gtt	gga	ggg	atg	aac	cgc	672
Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	
	210					215					220					
cgt	cca	att	tta	atc	att	gtt	act	ctg	gaa	acc	aga	gat	ggg	caa	gtc	720
Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	
225					230					235					240	
ctg	ggc	cga	cgc	tgc	ttt	gag	gcc	cgg	atc	tgt	gct	tgc	cca	gga	aga	768
Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	
				245					250					255		
gac	agg	aag	gcg	gat	gaa	gat	agc	atc	aga	aag	cag	caa	gtt	tcg	gac	816
Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	
			260					265					270			
agt	aca	aag	aac	ggt	gat	ggt	acg	aag	cgc	ccg	ttt	cgt	cag	aac	aca	864
Ser	Thr	Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	
		275					280					285				
cat	ggt	atc	cag	atg	aca	tcc	atc	aag	aaa	cga	aga	tcc	cca	gat	gat	912
His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	
	290					295					300					
gaa	ctg	tta	tac	tta	cca	gtg	agg	ggc	cgt	gag	act	tat	gaa	atg	ctg	960
Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	
305					310					315					320	
ttg	aag	atc	aaa	gag	tcc	ctg	gaa	ctc	atg	cag	tac	ctt	cct	cag	cac	1008
Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	
				325					330					335		

aca att gaa acg tac agg caa cag caa cag cag cag cac cag cac tta	1056
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu	
340 345 350	
ctt cag aaa cag acc tca ata cag tct cca tct tca tat ggt aac agc	1104
Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser	
355 360 365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tct gtg	1152
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val	
370 375 380	
agc cag ctt atc aac cct cag cag cgc aac gcc ctc act cct aca acc	1200
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr	
385 390 395 400	
att cct gat ggc atg gga gcc aac att ccc atg atg ggc acc cac atg	1248
Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met	
405 410 415	
cca atg gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct	1296
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro	
420 425 430	
ccc cca ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg	1344
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro	
435 440 445	
tat ccc aca gat tgc agc att gtc agt ttc tta gcg agg ttg ggc tgt	1392
Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys	
450 455 460	
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Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr	
465 470 475 480	
cag att gag cat tac tcc atg gat gat ctg gca agt ctg aaa atc cct	1488
Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro	
485 490 495	
gag caa ttt cga cat gcg atc tgg aag ggc atc ctg gac cac cgg cag	1536
Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln	
500 505 510	
ctc cac gaa ttc tcc tcc cct tct cat ctc ctg cgg acc cca agc agt	1584
Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser	
515 520 525	
gcc tct aca gtc agt gtg ggc tcc agt gag acc cgg ggt gag cgt gtt	1632
Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val	
530 535 540	
att gat gct gtg cga ttc acc ctc cgc cag acc atc tct ttc cca ccc	1680
Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro	
545 550 555 560	

cga gat gag tgg aat gac ttc aac ttt gac atg gat gct cgc cgc aat 1728
 Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
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aag caa cag cgc atc aaa gag gag ggg gag tga 1761
 Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585

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 <213> Homo sapiens

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 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac 96
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

ggc tcc tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc 144
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

gtc acg gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct 192
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

ctc tct cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg 240
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

cac agt ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc 288
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

acc tgg acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca 336
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

aag aca tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga 384
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

gct gtt atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg 432
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140

gag gtg gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac 480
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160

gag gga cag att gcc cct cct agt cat ttg att cga gta gag ggg aac	528
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
165 170 175	
agc cat gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtg	576
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
180 185 190	
ctg gta cct tat gag cca ccc cag gtt ggc act gaa ttc acg aca gtc	624
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195 200 205	
ttg tac aat ttc atg tgt aac agc agt tgt gtt gga ggg atg aac cgc	672
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210 215 220	
cgt cca att tta atc att gtt act ctg gaa acc aga gat ggg caa gtc	720
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val	
225 230 235 240	
ctg ggc cga cgc tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga	768
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg	
245 250 255	
gac agg aag gcg gat gaa gat agc atc aga aag cag caa gtt tcg gac	816
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp	
260 265 270	
agt aca aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca	864
Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr	
275 280 285	
cat ggt atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat	912
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp	
290 295 300	
gaa ctg tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg	960
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu	
305 310 315 320	
ttg aag atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac	1008
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His	
325 330 335	
aca att gaa acg tac agg caa cag caa cag cag cag cac cag cac tta	1056
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu	
340 345 350	
ctt cag aaa cag acc tca ata cag tct cca tct tca tat ggt aac agc	1104
Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser	
355 360 365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tct gtg	1152
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val	
370 375 380	

agc cag ctt atc aac cct cag cag cgc aac gcc ctc act cct aca acc 1200
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400

att cct gat ggc atg gga gcc aac att ccc atg atg ggc acc cac atg 1248
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

cca atg gct gga gac atg aat gga ctc agc ccc acc cag gca ctc cct 1296
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430

ccc cca ctc tcc atg cca tcc acc tcc cac tgc aca ccc cca cct ccg 1344
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
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tat ccc aca gat tgc agc att gtc agg atc tgg caa gtc tga 1386
 Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
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 <213> Homo sapiens

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tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac 96
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

ggc tcc tcg tcc acc agt ccc tat aac aca gac cac gcg cag aac agc 144
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

gtc acg gcg ccc tcg ccc tac gca cag ccc agc tcc acc ttc gat gct 192
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60

ctc tct cca tca ccc gcc atc ccc tcc aac acc gac tac cca ggc ccg 240
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80

cac agt ttc gac gtg tcc ttc cag cag tcg agc acc gcc aag tcg gcc 288
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95

acc tgg acg tat tcc act gaa ctg aag aaa ctc tac tgc caa att gca	336
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala	
100 105 110	
aag aca tgc ccc atc cag atc aag gtg atg acc cca cct cct cag gga	384
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly	
115 120 125	
gct gtt atc cgc gcc atg cct gtc tac aaa aaa gct gag cac gtc acg	432
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr	
130 135 140	
gag gtg gtg aag cgg tgc ccc aac cat gag ctg agc cgt gaa ttc aac	480
Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn	
145 150 155 160	
gag gga cag att gcc cct cct agt cat ttg att cga gta gag ggg aac	528
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
165 170 175	
agc cat gcc cag tat gta gaa gat ccc atc aca gga aga cag agt gtg	576
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
180 185 190	
ctg gta cct tat gag cca ccc cag gtt ggc act gaa ttc acg aca gtc	624
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195 200 205	
ttg tac aat ttc atg tgt aac agc agt tgt gtt gga ggg atg aac cgc	672
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210 215 220	
cgt cca att tta atc att gtt act ctg gaa acc aga gat ggg caa gtc	720
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val	
225 230 235 240	
ctg ggc cga cgc tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga	768
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg	
245 250 255	
gac agg aag gcg gat gaa gat agc atc aga aag cag caa gtt tcg gac	816
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp	
260 265 270	
agt aca aag aac ggt gat ggt acg aag cgc ccg ttt cgt cag aac aca	864
Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr	
275 280 285	
cat ggt atc cag atg aca tcc atc aag aaa cga aga tcc cca gat gat	912
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp	
290 295 300	
gaa ctg tta tac tta cca gtg agg ggc cgt gag act tat gaa atg ctg	960
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu	
305 310 315 320	

ttg aag atc aaa gag tcc ctg gaa ctc atg cag tac ctt cct cag cac	1008
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His	
325 330 335	

aca att gaa acg tac agg caa cag caa cag cag cag cac cag cac tta	1056
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu	
340 345 350	

ctt cag aaa cat ctc ctt tca gcc tgc ttc agg aat gag ctt gtg gag	1104
Leu Gln Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu	
355 360 365	

ccc cgg aga gaa act cca aaa caa tct gac gtc ttc ttt aga cat tcc	1152
Pro Arg Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser	
370 375 380	

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Lys Pro Pro Asn Arg Ser Val Tyr Pro	
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cct tac atc cag cgt ttc ata gaa acc cca gct cat ttc tcg tgg aaa	96
Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys	
20 25 30	

gaa agt tat tac aga tct gcc atg tcg cag agc acc cag aca agc gag	144
Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu	
35 40 45	

ttc ctc agc cca gag gtc ttc cag cat atc tgg gat ttt ctg gaa cag	192
Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln	
50 55 60	

cct ata tgc tca gta cag ccc atc gag ttg aac ttt gtg gat gaa cct	240
Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro	
65 70 75 80	

tcc gaa aat ggt gca aca aac aag att gag att agc atg gat tgt atc	288
Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile	
85 90 95	

cgc atg caa gac tca gac ctc agt gac ccc atg tgg cca cag tac acg	336
Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr	
100 105 110	
aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc	384
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser	
115 120 125	
tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc gtg acg	432
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr	
130 135 140	
gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc ctc tct	480
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser	
145 150 155 160	
cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca cac agc	528
Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser	
165 170 175	
ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc acc tgg	576
Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp	
180 185 190	
acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg aag aca	624
Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr	
195 200 205	
tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc gct gtt	672
Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val	
210 215 220	
atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc gag gtt	720
Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	
225 230 235 240	
gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat gag gga	768
Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly	
245 250 255	
cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac agc cat	816
Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His	
260 265 270	
gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg ctg gtc	864
Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val	
275 280 285	
cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc ctg tac	912
Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr	
290 295 300	
aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga cgt cca	960
Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro	
305 310 315 320	

att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc	1008
Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly	
325 330 335	
cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac cgg	1056
Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg	
340 345 350	
aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac agc gca	1104
Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala	
355 360 365	
aag aac ggc gat ggt acg aag cgc cct ttc cgt cag aat aca cac gga	1152
Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly	
370 375 380	
atc cag atg act tcc atc aag aaa cgg aga tcc cca gat gat gag ctg	1200
Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu	
385 390 395 400	
ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg ctg aag	1248
Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys	
405 410 415	
atc aaa gag tca ctg gag ctc atg cag tac ctc cct cag cac acg atc	1296
Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile	
420 425 430	
gaa acg tac agg cag cag cag cag cag cag cac cag cac cta ctt cag	1344
Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln	
435 440 445	
aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt tcc cca	1392
Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser Ser Pro	
450 455 460	
cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg agc cag	1440
Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln	
465 470 475 480	
ctt atc aac cca cag cag cgc aat gcc ctc act ccc acc acc atg cct	1488
Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Met Pro	
485 490 495	
gag ggc atg gga gcc aac att cct atg atg ggc act cac atg cca atg	1536
Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met	
500 505 510	
gct gga gac atg aat gga ctc agc cct acc caa gct ctc cct cct cca	1584
Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro	
515 520 525	
ctc tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc tac ccc	1632
Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro	
530 535 540	

aca gac tgc agc att gtc agt ttc tta gca agg ttg ggc tgc tca tca 1680
 Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser
 545 550 555 560

tgc ctg gac tat ttc acg acc cag ggg ctg acc acc atc tat cag att 1728
 Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile
 565 570 575

gag cat tac tcc atg gat gat ttg gca agt ctg aag atc cct gaa cag 1776
 Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln
 580 585 590

ttc cga cat gcc atc tgg aag ggc atc ctg gac cac agg cag ctg cac 1824
 Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His
 595 600 605

gac ttc tcc tca cct cct cat ctc ctg agg acc cca agt ggt gcc tct 1872
 Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly Ala Ser
 610 615 620

acc gtc agt gtg ggc tcc agt gag acc cgt ggt gaa cgt gtg atc gat 1920
 Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp
 625 630 635 640

gcc gtg cgc ttt acc ctc cgc cag acc atc tct ttt cca ccc cgt gac 1968
 Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp
 645 650 655

gag tgg aat gat ttc aac ttt gac atg gat tct cgt cgc aac aag cag 2016
 Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn Lys Gln
 660 665 670

cag cgt atc aaa gag gaa gga gaa tga 2043
 Gln Arg Ile Lys Glu Glu Gly Glu
 675 680

<210> 8
 <211> 1668
 <212> DNA
 <213> Murine sp.

<220>
 <221> CDS
 <222> (1)..(1665)

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 1 5 10 15

cct tac atc cag cgt ttc ata gaa acc cca gct cat ttc tcg tgg aaa 96
 Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30

gaa agt tat tac aga tct gcc atg tcg cag agc acc cag aca agc gag 144
 Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45

ttc ctc agc cca gag gtc ttc cag cat atc tgg gat ttt ctg gaa cag	192
Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln	
50 55 60	
cct ata tgc tca gta cag ccc atc gag ttg aac ttt gtg gat gaa cct	240
Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro	
65 70 75 80	
tcc gaa aat ggt gca aca aac aag att gag att agc atg gat tgt atc	288
Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile	
85 90 95	
cgc atg caa gac tca gac ctc agt gac ccc atg tgg cca cag tac acg	336
Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr	
100 105 110	
aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc	384
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser	
115 120 125	
tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc gtg acg	432
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr	
130 135 140	
gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc ctc tct	480
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser	
145 150 155 160	
cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca cac agc	528
Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser	
165 170 175	
ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc acc tgg	576
Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp	
180 185 190	
acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg aag aca	624
Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr	
195 200 205	
tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc gct gtt	672
Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val	
210 215 220	
atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc gag gtt	720
Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	
225 230 235 240	
gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat gag gga	768
Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly	
245 250 255	
cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac agc cat	816
Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His	
260 265 270	

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gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg ctg gtc 864
Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val
      275                      280                      285

cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc ctg tac 912
Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr
      290                      295                      300

aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga cgt cca 960
Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro
      305                      310                      315

att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc 1008
Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly
      325                      330                      335

cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac cgg 1056
Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg
      340                      345                      350

aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac agc gca 1104
Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala
      355                      360                      365

aag aac ggc gat ggt acg aag cgc cct ttc cgt cag aat aca cac gga 1152
Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr His Gly
      370                      375                      380

atc cag atg act tcc atc aag aaa cgg aga tcc cca gat gat gag ctg 1200
Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu
      385                      390                      395

ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg ctg aag 1248
Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys
      405                      410                      415

atc aaa gag tca ctg gag ctc atg cag tac ctc cct cag cac acg atc 1296
Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile
      420                      425                      430

gaa acg tac agg cag cag cag cag cag cag cac cag cac cta ctt cag 1344
Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln
      435                      440                      445

aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt tcc cca 1392
Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser Ser Pro
      450                      455                      460

cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg agc cag 1440
Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln
      465                      470                      475

ctt atc aac cca cag cag cgc aat gcc ctc act ccc acc acc atg cct 1488
Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Met Pro
      485                      490                      495

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gag ggc atg gga gcc aac att cct atg atg ggc act cac atg cca atg 1536
 Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met
 500 505 510

gct gga gac atg aat gga ctc agc cct acc caa gct ctc cct cct cca 1584
 Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro
 515 520 525

ctc tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc tac ccc 1632
 Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro
 530 535 540

aca gac tgc agc att gtc agg att tgg caa gtc tga 1668
 Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 545 550 555

<210> 9
 <211> 1452
 <212> DNA
 <213> Murine sp.

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 <221> CDS
 <222> (1)..(1449)

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 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15

cct tac atc cag cgt ttc ata gaa acc cca gct cat ttc tcg tgg aaa 96
 Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30

gaa agt tat tac aga tct gcc atg tcg cag agc acc cag aca agc gag 144
 Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45

ttc ctc agc cca gag gtc ttc cag cat atc tgg gat ttt ctg gaa cag 192
 Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60

cct ata tgc tca gta cag ccc atc gag ttg aac ttt gtg gat gaa cct 240
 Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
 65 70 75 80

tcc gaa aat ggt gca aca aac aag att gag att agc atg gat tgt atc 288
 Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
 85 90 95

cgc atg caa gac tca gac ctc agt gac ccc atg tgg cca cag tac acg 336
 Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
 100 105 110

aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac ggc tcc	384
Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser	
115 120 125	
tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc gtg acg	432
Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr	
130 135 140	
gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc ctc tct	480
Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser	
145 150 155 160	
cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca cac agc	528
Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser	
165 170 175	
ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc acc tgg	576
Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp	
180 185 190	
acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg aag aca	624
Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr	
195 200 205	
tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc gct gtt	672
Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val	
210 215 220	
atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc gag gtt	720
Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val	
225 230 235 240	
gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat gag gga	768
Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly	
245 250 255	
cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac agc cat	816
Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His	
260 265 270	
gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg ctg gtc	864
Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val	
275 280 285	
cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc ctg tac	912
Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr	
290 295 300	
aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga cgt cca	960
Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro	
305 310 315 320	
att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc ctg ggc	1008
Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly	
325 330 335	

cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga gac cgg	1056
Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg	
340 345 350	
aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac agc gca	1104
Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala	
355 360 365	
aag aac ggc gat gct ttc cgt cag aat aca cac gga atc cag atg act	1152
Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr	
370 375 380	
tcc atc aag aaa cgg aga tcc cca gat gat gag ctg ctg tac cta cca	1200
Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro	
385 390 395 400	
gtg aga ggt cgt gag acg tac gag atg ttg ctg aag atc aaa gag tca	1248
Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser	
405 410 415	
ctg gag ctc atg cag tac ctc cct cag cac acg atc gaa acg tac agg	1296
Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg	
420 425 430	
cag cag cag cag cag cag cac cag cac cta ctt cag aaa cat ctc ctt	1344
Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu	
435 440 445	
tca gcc tgc ttc agg aat gag ctt gtg gag ccc cgg gga gaa gct ccg	1392
Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu Ala Pro	
450 455 460	
aca cag tct gac gtc ttc ttt aga cat tcc aac ccc cca aac cac tcc	1440
Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn His Ser	
465 470 475 480	
gtg tac cca tag	1452
Val Tyr Pro	
<p><210> 10</p> <p><211> 1761</p> <p><212> DNA</p> <p><213> Murine sp.</p>	
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Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln	
1 5 10 15	
tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac	96
Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn	
20 25 30	

ggc tcc tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc	144
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser	
35 40 45	
gtg acg gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc	192
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala	
50 55 60	
ctc tct cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca	240
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro	
65 70 75 80	
cac agc ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc	288
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala	
85 90 95	
acc tgg acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg	336
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala	
100 105 110	
aag aca tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc	384
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly	
115 120 125	
gct gtt atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc	432
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr	
130 135 140	
gag gtt gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat	480
Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn	
145 150 155 160	
gag gga cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac	528
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
165 170 175	
agc cat gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg	576
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
180 185 190	
ctg gtc cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc	624
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195 200 205	
ctg tac aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga	672
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210 215 220	
cgt cca att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc	720
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val	
225 230 235 240	
ctg ggc cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga	768
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg	
245 250 255	

gac cgg aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac	816
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp	
260 265 270	
agc gca aag aac ggc gat ggt acg aag cgc cct ttc cgt cag aat aca	864
Ser Ala Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr	
275 280 285	
cac gga atc cag atg act tcc atc aag aaa cgg aga tcc cca gat gat	912
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp	
290 295 300	
gag ctg ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg	960
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu	
305 310 315 320	
ctg aag atc aaa gag tca ctg gag ctc atg cag tac ctc cct cag cac	1008
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His	
325 330 335	
acg atc gaa acg tac agg cag cag cag cag cag cag cac cag cac cta	1056
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu	
340 345 350	
ctt cag aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt	1104
Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser	
355 360 365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg	1152
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val	
370 375 380	
agc cag ctt atc aac cca cag cag cgc aat gcc ctc act ccc acc acc	1200
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr	
385 390 395 400	
atg cct gag ggc atg gga gcc aac att cct atg atg ggc act cac atg	1248
Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met	
405 410 415	
cca atg gct gga gac atg aat gga ctc agc cct acc caa gct ctc cct	1296
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro	
420 425 430	
cct cca ctc tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc	1344
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro	
435 440 445	
tac ccc aca gac tgc agc att gtc agt ttc tta gca agg ttg ggc tgc	1392
Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys	
450 455 460	
tca tca tgc ctg gac tat ttc acg acc cag ggg ctg acc acc atc tat	1440
Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr	
465 470 475 480	

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cag att gag cat tac tcc atg gat gat ttg gca agt ctg aag atc cct 1488
Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
               485                     490                     495

gaa cag ttc cga cat gcc atc tgg aag ggc atc ctg gac cac agg cag 1536
Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
               500                     505                     510

ctg cac gac ttc tcc tca cct cct cat ctc ctg agg acc cca agt ggt 1584
Leu His Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly
               515                     520                     525

gcc tct acc gtc agt gtg ggc tcc agt gag acc cgt ggt gaa cgt gtg 1632
Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
               530                     535                     540

atc gat gcc gtg cgc ttt acc ctc cgc cag acc atc tct ttt cca ccc 1680
Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
               545                     550                     555                     560

cgt gac gag tgg aat gat ttc aac ttt gac atg gat tct cgt cgc aac 1728
Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn
               565                     570                     575

aag cag cag cgt atc aaa gag gaa gga gaa tga 1761
Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
               580                     585

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<210> 11
<211> 1386
<212> DNA
<213> Murine sp.

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<220>
<221> CDS
<222> (1)..(1383)

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   1               5               10               15

tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac 96
Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
               20               25               30

ggc tcc tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc 144
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
               35               40               45

gtg acg gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc 192
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
   50               55               60

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ctc tct cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca	240
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro	
65 70 75 80	
cac agc ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc	288
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala	
85 90 95	
acc tgg acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg	336
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala	
100 105 110	
aag aca tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc	384
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly	
115 120 125	
gct gtt atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc	432
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr	
130 135 140	
gag gtt gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat	480
Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn	
145 150 155 160	
gag gga cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac	528
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
165 170 175	
agc cat gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg	576
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
180 185 190	
ctg gtc cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc	624
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195 200 205	
ctg tac aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga	672
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210 215 220	
cgt cca att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc	720
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val	
225 230 235 240	
ctg ggc cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga	768
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg	
245 250 255	
gac cgg aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac	816
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp	
260 265 270	
agc gca aag aac ggc gat ggt acg aag cgc cct ttc cgt cag aat aca	864
Ser Ala Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr	
275 280 285	

cac gga atc cag atg act tcc atc aag aaa cgg aga tcc cca gat gat	912
His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp	
290 295 300	
gag ctg ctg tac cta cca gtg aga ggt cgt gag acg tac gag atg ttg	960
Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu	
305 310 315 320	
ctg aag atc aaa gag tca ctg gag ctg atg cag tac ctg cct cag cac	1008
Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His	
325 330 335	
acg atc gaa acg tac agg cag cag cag cag cag cag cac cag cac cta	1056
Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu	
340 345 350	
ctt cag aaa cag acc tcg atg cag tct cag tct tca tat ggc aac agt	1104
Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser	
355 360 365	
tcc cca cct ctg aac aaa atg aac agc atg aac aag ctg cct tcc gtg	1152
Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val	
370 375 380	
agc cag ctt atc aac cca cag cag cgc aat gcc ctg act ccc acc acc	1200
Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr	
385 390 395 400	
atg cct gag ggc atg gga gcc aac att cct atg atg ggc act cac atg	1248
Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met	
405 410 415	
cca atg gct gga gac atg aat gga ctg agc cct acc caa gct ctg cct	1296
Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro	
420 425 430	
cct cca ctg tcc atg ccc tcc acc tcc cac tgc acc cca cca ccg ccc	1344
Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro	
435 440 445	
tac ccc aca gac tgc agc att gtc agg att tgg caa gtc tga	1386
Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val	
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<210> 12
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 <212> DNA
 <213> Murine sp.

<220>
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<400> 12

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Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln	
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tac acg aac ctg ggg ctc ctg aac agc atg gac cag cag att cag aac	96
Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn	
20 25 30	
ggc tcc tcg tcc acc agc ccc tac aac aca gac cac gca cag aat agc	144
Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser	
35 40 45	
gtg acg gcg ccc tcg ccc tat gca cag ccc agc tcc acc ttt gat gcc	192
Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala	
50 55 60	
ctc tct cca tcc cct gcc att ccc tcc aac aca gat tac ccg ggc cca	240
Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro	
65 70 75 80	
cac agc ttc gat gtg tcc ttc cag cag tca agc act gcc aag tca gcc	288
His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala	
85 90 95	
acc tgg acg tat tcc acc gaa ctg aag aag ctg tac tgc cag att gcg	336
Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala	
100 105 110	
aag aca tgc ccc atc cag atc aag gtg atg acc cca ccc cca cag ggc	384
Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly	
115 120 125	
gct gtt atc cgt gcc atg cct gtc tac aag aaa gct gag cat gtc acc	432
Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr	
130 135 140	
gag gtt gtg aaa cga tgc cct aac cat gag ctg agc cgt gag ttc aat	480
Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn	
145 150 155 160	
gag gga cag att gcc cct ccc agt cat ctg att cga gta gaa ggg aac	528
Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn	
165 170 175	
agc cat gcc cag tat gta gaa gat cct atc acg gga agg cag agc gtg	576
Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val	
180 185 190	
ctg gtc cct tat gag cca cca cag gtt ggc act gaa ttc aca aca gtc	624
Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val	
195 200 205	
ctg tac aat ttc atg tgt aac agc agc tgc gtc gga gga atg aac aga	672
Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg	
210 215 220	

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cgt cca att tta atc atc gtt act ctg gaa acc aga gat ggg caa gtc 720
Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
225                230                235                240

ctg ggc cga cgg tgc ttt gag gcc cgg atc tgt gct tgc cca gga aga 768
Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
                245                250                255

gac cgg aag gca gat gaa gac agc atc aga aag cag caa gta tcg gac 816
Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
                260                265                270

agc gca aag aac ggc gat gct ttc cgt cag aat aca cac gga atc cag 864
Ser Ala Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln
                275                280                285

atg act tcc atc aag aaa cgg aga tcc cca gat gat gag ctg ctg tac 912
Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr
                290                295                300

cta cca gtg aga ggt cgt gag acg tac gag atg ttg ctg aag atc aaa 960
Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys
305                310                315                320

gag tca ctg gag ctc atg cag tac ctc cct cag cac acg atc gaa acg 1008
Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr
                325                330                335

tac agg cag cag cag cag cag cag cag cac cag cac cta ctt cag aaa cat 1056
Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His
                340                345                350

ctc ctt tca gcc tgc ttc agg aat gag ctt gtg gag ccc cgg gga gaa 1104
Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu
                355                360                365

gct ccg aca cag tct gac gtc ttc ttt aga cat tcc aac ccc cca aac 1152
Ala Pro Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn
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cac tcc gtg tac cca tag 1170
His Ser Val Tyr Pro
385

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<210> 13

<211> 641

<212> PRT

<213> Homo sapiens

<400> 13

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Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
  1              5              10              15

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Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
      20              25              30

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Ile	Asp	Leu	Asn	Phe	Val	Asp	Glu	Pro	Ser	Glu	Asp	Gly	Ala	Thr	Asn
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Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	Arg	Met	Gln	Asp	Ser	Asp	Leu
	50					55					60				
Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	Asn	Leu	Gly	Leu	Leu	Asn	Ser
	65				70					75					80
Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser	Ser	Ser	Thr	Ser	Pro	Tyr	Asn
				85					90					95	
Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln
			100					105					110		
Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser
		115					120					125			
Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln
	130					135					140				
Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys
	145				150					155					160
Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val
				165					170					175	
Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr
			180					185					190		
Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His
		195					200					205			
Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His
	210					215					220				
Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro
	225				230					235					240
Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val
				245					250					255	
Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser
			260					265					270		
Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu
		275					280					285			
Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg
	290					295					300				
Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile
	305				310					315					320
Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Thr	Lys	Asn	Gly	Asp	Gly	Thr	Lys
				325					330					335	

Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys
			340					345					350		
Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly
			355				360					365			
Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu
	370					375					380				
Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln
385					390					395					400
Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln	Lys	Gln	Thr	Ser	Ile	Gln	Ser
				405					410					415	
Pro	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro	Pro	Leu	Asn	Lys	Met	Asn	Ser
			420					425					430		
Met	Asn	Lys	Leu	Pro	Ser	Val	Ser	Gln	Leu	Ile	Asn	Pro	Gln	Gln	Arg
		435					440					445			
Asn	Ala	Leu	Thr	Pro	Thr	Thr	Ile	Pro	Asp	Gly	Met	Gly	Ala	Asn	Ile
	450					455					460				
Pro	Met	Met	Gly	Thr	His	Met	Pro	Met	Ala	Gly	Asp	Met	Asn	Gly	Leu
465					470					475					480
Ser	Pro	Thr	Gln	Ala	Leu	Pro	Pro	Pro	Leu	Ser	Met	Pro	Ser	Thr	Ser
				485					490					495	
His	Cys	Thr	Pro	Pro	Pro	Pro	Tyr	Pro	Thr	Asp	Cys	Ser	Ile	Val	Ser
			500					505					510		
Phe	Leu	Ala	Arg	Leu	Gly	Cys	Ser	Ser	Cys	Leu	Asp	Tyr	Phe	Thr	Thr
		515					520					525			
Gln	Gly	Leu	Thr	Thr	Ile	Tyr	Gln	Ile	Glu	His	Tyr	Ser	Met	Asp	Asp
	530					535					540				
Leu	Ala	Ser	Leu	Lys	Ile	Pro	Glu	Gln	Phe	Arg	His	Ala	Ile	Trp	Lys
545					550					555					560
Gly	Ile	Leu	Asp	His	Arg	Gln	Leu	His	Glu	Phe	Ser	Ser	Pro	Ser	His
				565					570					575	
Leu	Leu	Arg	Thr	Pro	Ser	Ser	Ala	Ser	Thr	Val	Ser	Val	Gly	Ser	Ser
			580					585					590		
Glu	Thr	Arg	Gly	Glu	Arg	Val	Ile	Asp	Ala	Val	Arg	Phe	Thr	Leu	Arg
		595					600					605			
Gln	Thr	Ile	Ser	Phe	Pro	Pro	Arg	Asp	Glu	Trp	Asn	Asp	Phe	Asn	Phe
	610					615					620				
Asp	Met	Asp	Ala	Arg	Arg	Asn	Lys	Gln	Gln	Arg	Ile	Lys	Glu	Glu	Gly
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Glu

<210> 14

<211> 516

<212> PRT

<213> Homo sapiens

<400> 14

Met	Ser	Gln	Ser	Thr	Gln	Thr	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Val	Phe
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Gln	His	Ile	Trp	Asp	Phe	Leu	Glu	Gln	Pro	Ile	Cys	Ser	Val	Gln	Pro
			20					25					30		
Ile	Asp	Leu	Asn	Phe	Val	Asp	Glu	Pro	Ser	Glu	Asp	Gly	Ala	Thr	Asn
		35					40					45			
Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	Arg	Met	Gln	Asp	Ser	Asp	Leu
	50					55					60				
Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	Asn	Leu	Gly	Leu	Leu	Asn	Ser
	65				70					75					80
Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser	Ser	Ser	Thr	Ser	Pro	Tyr	Asn
				85					90					95	
Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln
		100						105					110		
Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser
		115					120					125			
Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln
	130					135					140				
Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys
	145				150					155					160
Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val
			165						170					175	
Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr
		180						185					190		
Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His
		195					200					205			
Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His
	210					215					220				
Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro
	225				230					235					240
Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val
				245					250					255	

Gly Thr Glu Phe Thr Thr Val Leu Tyr Asn Phe Met Cys Asn Ser Ser
 260 265 270
 Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Val Thr Leu
 275 280 285
 Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Cys Phe Glu Ala Arg
 290 295 300
 Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr Ser Ile Gln Ser
 405 410 415
 Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn Lys Met Asn Ser
 420 425 430
 Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn Pro Gln Gln Arg
 435 440 445
 Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met Gly Ala Asn Ile
 450 455 460
 Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp Met Asn Gly Leu
 465 470 475 480
 Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met Pro Ser Thr Ser
 485 490 495
 His Cys Thr Pro Pro Pro Tyr Pro Thr Asp Cys Ser Ile Val Arg
 500 505 510
 Ile Trp Gln Val
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<210> 15
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 15

Met	Ser	Gln	Ser	Thr	Gln	Thr	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Val	Phe
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Gln	His	Ile	Trp	Asp	Phe	Leu	Glu	Gln	Pro	Ile	Cys	Ser	Val	Gln	Pro
			20					25					30		
Ile	Asp	Leu	Asn	Phe	Val	Asp	Glu	Pro	Ser	Glu	Asp	Gly	Ala	Thr	Asn
		35					40					45			
Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	Arg	Met	Gln	Asp	Ser	Asp	Leu
	50					55					60				
Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	Asn	Leu	Gly	Leu	Leu	Asn	Ser
65					70					75					80
Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser	Ser	Ser	Thr	Ser	Pro	Tyr	Asn
				85					90					95	
Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln
			100					105					110		
Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser
		115					120					125			
Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln
	130					135					140				
Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys
145				150						155					160
Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val
			165						170					175	
Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr
		180						185					190		
Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His
		195					200					205			
Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His
	210					215					220				
Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro
225					230					235					240
Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val
			245						250					255	
Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser
			260					265					270		
Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu
		275					280					285			
Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg
					295						300				

Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp Ser Ile
 305 310 315 320
 Arg Lys Gln Gln Val Ser Asp Ser Thr Lys Asn Gly Asp Gly Thr Lys
 325 330 335
 Arg Pro Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr Ser Ile Lys
 340 345 350
 Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro Val Arg Gly
 355 360 365
 Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser Leu Glu Leu
 370 375 380
 Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg Gln Gln Gln
 385 390 395 400
 Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu Ser Ala Cys
 405 410 415
 Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr Pro Lys Gln Ser
 420 425 430
 Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg Ser Val Tyr Pro
 435 440 445

<210> 16
 <211> 586
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
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 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110

Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Ile Pro Asp Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415

Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
420 425 430

Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
435 440 445

Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
450 455 460

Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
465 470 475 480

Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
485 490 495

Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
500 505 510

Leu His Glu Phe Ser Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser
515 520 525

Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
530 535 540

Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
545 550 555 560

Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn
565 570 575

Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
580 585

<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17
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Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
35 40 45

Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
50 55 60

Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
65 70 75 80

His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
85 90 95

Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala		
			100					105					110				
Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Pro	Gln	Gly		
		115					120					125					
Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr		
	130					135					140						
Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn		
145					150					155					160		
Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn		
				165					170					175			
Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val		
			180					185					190				
Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val		
		195					200					205					
Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg		
	210					215					220						
Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val		
225					230					235					240		
Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg		
				245					250					255			
Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp		
			260					265					270				
Ser	Thr	Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr		
		275					280					285					
His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp		
	290					295					300						
Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu		
305					310					315					320		
Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His		
				325					330					335			
Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu		
			340					345					350				
Leu	Gln	Lys	Gln	Thr	Ser	Ile	Gln	Ser	Pro	Ser	Ser	Tyr	Gly	Asn	Ser		
		355					360					365					
Ser	Pro	Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val		
	370					375					380						
Ser	Gln	Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr		
385					390					395					400		

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
195 200 205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Thr Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335
 Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys His Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu
 355 360 365
 Pro Arg Arg Glu Thr Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser
 370 375 380
 Lys Pro Pro Asn Arg Ser Val Tyr Pro
 385 390

<210> 19
 <211> 680
 <212> PRT
 <213> Murine sp.

<400> 19
 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15
 Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30
 Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45
 Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60
 Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
 65 70 75 80

Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu	385	390	395	400
Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys	405	410	415	
Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile	420	425	430	
Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln	435	440	445	
Lys	Gln	Thr	Ser	Met	Gln	Ser	Gln	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro	450	455	460	
Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val	Ser	Gln	465	470	475	480
Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr	Met	Pro	485	490	495	
Glu	Gly	Met	Gly	Ala	Asn	Ile	Pro	Met	Met	Gly	Thr	His	Met	Pro	Met	500	505	510	
Ala	Gly	Asp	Met	Asn	Gly	Leu	Ser	Pro	Thr	Gln	Ala	Leu	Pro	Pro	Pro	515	520	525	
Leu	Ser	Met	Pro	Ser	Thr	Ser	His	Cys	Thr	Pro	Pro	Pro	Pro	Tyr	Pro	530	535	540	
Thr	Asp	Cys	Ser	Ile	Val	Ser	Phe	Leu	Ala	Arg	Leu	Gly	Cys	Ser	Ser	545	550	555	560
Cys	Leu	Asp	Tyr	Phe	Thr	Thr	Gln	Gly	Leu	Thr	Thr	Ile	Tyr	Gln	Ile	565	570	575	
Glu	His	Tyr	Ser	Met	Asp	Asp	Leu	Ala	Ser	Leu	Lys	Ile	Pro	Glu	Gln	580	585	590	
Phe	Arg	His	Ala	Ile	Trp	Lys	Gly	Ile	Leu	Asp	His	Arg	Gln	Leu	His	595	600	605	
Asp	Phe	Ser	Ser	Pro	Pro	His	Leu	Leu	Arg	Thr	Pro	Ser	Gly	Ala	Ser	610	615	620	
Thr	Val	Ser	Val	Gly	Ser	Ser	Glu	Thr	Arg	Gly	Glu	Arg	Val	Ile	Asp	625	630	635	640
Ala	Val	Arg	Phe	Thr	Leu	Arg	Gln	Thr	Ile	Ser	Phe	Pro	Pro	Arg	Asp	645	650	655	
Glu	Trp	Asn	Asp	Phe	Asn	Phe	Asp	Met	Asp	Ser	Arg	Arg	Asn	Lys	Gln	660	665	670	
Gln	Arg	Ile	Lys	Glu	Glu	Gly	Glu									675	680		

<210> 20
 <211> 555
 <212> PRT
 <213> Murine sp.

<400> 20

Met	Asn	Phe	Glu	Thr	Ser	Arg	Cys	Ala	Thr	Leu	Gln	Tyr	Cys	Pro	Asp	1	5	10	15
Pro	Tyr	Ile	Gln	Arg	Phe	Ile	Glu	Thr	Pro	Ala	His	Phe	Ser	Trp	Lys	20	25	30	
Glu	Ser	Tyr	Tyr	Arg	Ser	Ala	Met	Ser	Gln	Ser	Thr	Gln	Thr	Ser	Glu	35	40	45	
Phe	Leu	Ser	Pro	Glu	Val	Phe	Gln	His	Ile	Trp	Asp	Phe	Leu	Glu	Gln	50	55	60	
Pro	Ile	Cys	Ser	Val	Gln	Pro	Ile	Glu	Leu	Asn	Phe	Val	Asp	Glu	Pro	65	70	75	80
Ser	Glu	Asn	Gly	Ala	Thr	Asn	Lys	Ile	Glu	Ile	Ser	Met	Asp	Cys	Ile	85	90	95	
Arg	Met	Gln	Asp	Ser	Asp	Leu	Ser	Asp	Pro	Met	Trp	Pro	Gln	Tyr	Thr	100	105	110	
Asn	Leu	Gly	Leu	Leu	Asn	Ser	Met	Asp	Gln	Gln	Ile	Gln	Asn	Gly	Ser	115	120	125	
Ser	Ser	Thr	Ser	Pro	Tyr	Asn	Thr	Asp	His	Ala	Gln	Asn	Ser	Val	Thr	130	135	140	
Ala	Pro	Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Ala	Leu	Ser	145	150	155	160
Pro	Ser	Pro	Ala	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	Ser	165	170	175	
Phe	Asp	Val	Ser	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	180	185	190	
Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	195	200	205	
Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Pro	Gln	Gly	Ala	Val	210	215	220	
Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Glu	Val	225	230	235	240
Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	Glu	Gly	245	250	255	

Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Ser	His	260	265	270
Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	Leu	Val	275	280	285
Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	Leu	Tyr	290	295	300
Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	305	310	315
Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	325	330	335
Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	340	345	350
Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	Ser	Ala	355	360	365
Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	His	Gly	370	375	380
Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	Glu	Leu	385	390	395
Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	Leu	Lys	405	410	415
Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	Thr	Ile	420	425	430
Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	Leu	Gln	435	440	445
Lys	Gln	Thr	Ser	Met	Gln	Ser	Gln	Ser	Ser	Tyr	Gly	Asn	Ser	Ser	Pro	450	455	460
Pro	Leu	Asn	Lys	Met	Asn	Ser	Met	Asn	Lys	Leu	Pro	Ser	Val	Ser	Gln	465	470	475
Leu	Ile	Asn	Pro	Gln	Gln	Arg	Asn	Ala	Leu	Thr	Pro	Thr	Thr	Met	Pro	485	490	495
Glu	Gly	Met	Gly	Ala	Asn	Ile	Pro	Met	Met	Gly	Thr	His	Met	Pro	Met	500	505	510
Ala	Gly	Asp	Met	Asn	Gly	Leu	Ser	Pro	Thr	Gln	Ala	Leu	Pro	Pro	Pro	515	520	525
Leu	Ser	Met	Pro	Ser	Thr	Ser	His	Cys	Thr	Pro	Pro	Pro	Pro	Tyr	Pro	530	535	540
Thr	Asp	Cys	Ser	Ile	Val	Arg	Ile	Trp	Gln	Val						545	550	555

<210> 21
 <211> 483
 <212> PRT
 <213> Murine sp.

<400> 21
 Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
 1 5 10 15
 Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
 20 25 30
 Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
 35 40 45
 Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
 50 55 60
 Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
 65 70 75 80
 Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
 85 90 95
 Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
 100 105 110
 Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn Gly Ser
 115 120 125
 Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser Val Thr
 130 135 140
 Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala Leu Ser
 145 150 155 160
 Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His Ser
 165 170 175
 Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp
 180 185 190
 Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr
 195 200 205
 Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly Ala Val
 210 215 220
 Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Glu Val
 225 230 235 240
 Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn Glu Gly
 245 250 255
 Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn Ser His
 260 265 270

Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val Leu Val
 275 280 285
 Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val Leu Tyr
 290 295 300
 Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro
 305 310 315 320
 Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly
 325 330 335
 Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg
 340 345 350
 Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp Ser Ala
 355 360 365
 Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln Met Thr
 370 375 380
 Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr Leu Pro
 385 390 395 400
 Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys Glu Ser
 405 410 415
 Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr Tyr Arg
 420 425 430
 Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu Leu
 435 440 445
 Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu Ala Pro
 450 455 460
 Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn His Ser
 465 470 475 480
 Val Tyr Pro

<210> 22
 <211> 586
 <212> PRT
 <213> Murine sp.

<400> 22
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45

Val	Thr	Ala	Pro	Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Ala	50	55	60	
Leu	Ser	Pro	Ser	Pro	Ala	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	65	70	75	80
His	Ser	Phe	Asp	Val	Ser	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	85	90	95	
Thr	Trp	Thr	Tyr	Ser	Thr	Glu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	100	105	110	
Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	Val	Met	Thr	Pro	Pro	Pro	Gln	Gly	115	120	125	
Ala	Val	Ile	Arg	Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	130	135	140	
Glu	Val	Val	Lys	Arg	Cys	Pro	Asn	His	Glu	Leu	Ser	Arg	Glu	Phe	Asn	145	150	155	160
Glu	Gly	Gln	Ile	Ala	Pro	Pro	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	165	170	175	
Ser	His	Ala	Gln	Tyr	Val	Glu	Asp	Pro	Ile	Thr	Gly	Arg	Gln	Ser	Val	180	185	190	
Leu	Val	Pro	Tyr	Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Val	195	200	205	
Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	210	215	220	
Arg	Pro	Ile	Leu	Ile	Ile	Val	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	225	230	235	240
Leu	Gly	Arg	Arg	Cys	Phe	Glu	Ala	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	245	250	255	
Asp	Arg	Lys	Ala	Asp	Glu	Asp	Ser	Ile	Arg	Lys	Gln	Gln	Val	Ser	Asp	260	265	270	
Ser	Ala	Lys	Asn	Gly	Asp	Gly	Thr	Lys	Arg	Pro	Phe	Arg	Gln	Asn	Thr	275	280	285	
His	Gly	Ile	Gln	Met	Thr	Ser	Ile	Lys	Lys	Arg	Arg	Ser	Pro	Asp	Asp	290	295	300	
Glu	Leu	Leu	Tyr	Leu	Pro	Val	Arg	Gly	Arg	Glu	Thr	Tyr	Glu	Met	Leu	305	310	315	320
Leu	Lys	Ile	Lys	Glu	Ser	Leu	Glu	Leu	Met	Gln	Tyr	Leu	Pro	Gln	His	325	330	335	
Thr	Ile	Glu	Thr	Tyr	Arg	Gln	Gln	Gln	Gln	Gln	Gln	His	Gln	His	Leu	340	345	350	

Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys
 450 455 460
 Ser Ser Cys Leu Asp Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr
 465 470 475 480
 Gln Ile Glu His Tyr Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro
 485 490 495
 Glu Gln Phe Arg His Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln
 500 505 510
 Leu His Asp Phe Ser Ser Pro Pro His Leu Leu Arg Thr Pro Ser Gly
 515 520 525
 Ala Ser Thr Val Ser Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val
 530 535 540
 Ile Asp Ala Val Arg Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro
 545 550 555 560
 Arg Asp Glu Trp Asn Asp Phe Asn Phe Asp Met Asp Ser Arg Arg Asn
 565 570 575
 Lys Gln Gln Arg Ile Lys Glu Glu Gly Glu
 580 585

<210> 23
 <211> 461
 <212> PRT
 <213> Murine sp.

<400> 23
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30

Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125
 Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
 130 135 140
 Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
 145 150 155 160
 Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
 165 170 175
 Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
 180 185 190
 Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
 195 200 205
 Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
 210 215 220
 Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
 225 230 235 240
 Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
 245 250 255
 Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
 260 265 270
 Ser Ala Lys Asn Gly Asp Gly Thr Lys Arg Pro Phe Arg Gln Asn Thr
 275 280 285
 His Gly Ile Gln Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp
 290 295 300
 Glu Leu Leu Tyr Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu
 305 310 315 320
 Leu Lys Ile Lys Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His
 325 330 335

Thr Ile Glu Thr Tyr Arg Gln Gln Gln Gln Gln His Gln His Leu
 340 345 350
 Leu Gln Lys Gln Thr Ser Met Gln Ser Gln Ser Ser Tyr Gly Asn Ser
 355 360 365
 Ser Pro Pro Leu Asn Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val
 370 375 380
 Ser Gln Leu Ile Asn Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr
 385 390 395 400
 Met Pro Glu Gly Met Gly Ala Asn Ile Pro Met Met Gly Thr His Met
 405 410 415
 Pro Met Ala Gly Asp Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro
 420 425 430
 Pro Pro Leu Ser Met Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro
 435 440 445
 Tyr Pro Thr Asp Cys Ser Ile Val Arg Ile Trp Gln Val
 450 455 460

<210> 24
 <211> 389
 <212> PRT
 <213> Murine sp.

<400> 24
 Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15
 Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met Asp Gln Gln Ile Gln Asn
 20 25 30
 Gly Ser Ser Ser Thr Ser Pro Tyr Asn Thr Asp His Ala Gln Asn Ser
 35 40 45
 Val Thr Ala Pro Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Ala
 50 55 60
 Leu Ser Pro Ser Pro Ala Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro
 65 70 75 80
 His Ser Phe Asp Val Ser Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala
 85 90 95
 Thr Trp Thr Tyr Ser Thr Glu Leu Lys Lys Leu Tyr Cys Gln Ile Ala
 100 105 110
 Lys Thr Cys Pro Ile Gln Ile Lys Val Met Thr Pro Pro Pro Gln Gly
 115 120 125

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Ala Val Ile Arg Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr
130                               135                               140

Glu Val Val Lys Arg Cys Pro Asn His Glu Leu Ser Arg Glu Phe Asn
145                               150                               155                               160

Glu Gly Gln Ile Ala Pro Pro Ser His Leu Ile Arg Val Glu Gly Asn
                               165                               170                               175

Ser His Ala Gln Tyr Val Glu Asp Pro Ile Thr Gly Arg Gln Ser Val
                               180                               185                               190

Leu Val Pro Tyr Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Val
                               195                               200                               205

Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg
210                               215                               220

Arg Pro Ile Leu Ile Ile Val Thr Leu Glu Thr Arg Asp Gly Gln Val
225                               230                               235                               240

Leu Gly Arg Arg Cys Phe Glu Ala Arg Ile Cys Ala Cys Pro Gly Arg
                               245                               250                               255

Asp Arg Lys Ala Asp Glu Asp Ser Ile Arg Lys Gln Gln Val Ser Asp
                               260                               265                               270

Ser Ala Lys Asn Gly Asp Ala Phe Arg Gln Asn Thr His Gly Ile Gln
                               275                               280                               285

Met Thr Ser Ile Lys Lys Arg Arg Ser Pro Asp Asp Glu Leu Leu Tyr
290                               295                               300

Leu Pro Val Arg Gly Arg Glu Thr Tyr Glu Met Leu Leu Lys Ile Lys
305                               310                               315                               320

Glu Ser Leu Glu Leu Met Gln Tyr Leu Pro Gln His Thr Ile Glu Thr
                               325                               330                               335

Tyr Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His
                               340                               345                               350

Leu Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Gly Glu
                               355                               360                               365

Ala Pro Thr Gln Ser Asp Val Phe Phe Arg His Ser Asn Pro Pro Asn
                               370                               375                               380

His Ser Val Tyr Pro
385

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<210> 25
<211> 393
<212> PRT
<213> Homo sapiens

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<400> 25

Met	Glu	Glu	Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser	Gln
1				5					10					15	
Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn	Val	Leu
			20					25					30		
Ser	Pro	Leu	Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu	Ser	Pro	Asp
		35					40					45			
Asp	Ile	Glu	Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro	Asp	Glu	Ala	Pro
	50					55					60				
Arg	Met	Pro	Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Pro	Ala	Ala	Pro
65					70				75						80
Thr	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Pro	Ser	Trp	Pro	Leu	Ser	Ser	Ser
				85					90					95	
Val	Pro	Ser	Gln	Lys	Thr	Tyr	Gln	Gly	Ser	Tyr	Gly	Phe	Arg	Leu	Gly
			100					105					110		
Phe	Leu	His	Ser	Gly	Thr	Ala	Lys	Ser	Val	Thr	Cys	Thr	Tyr	Ser	Pro
		115					120					125			
Ala	Leu	Asn	Lys	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr	Cys	Pro	Val	Gln
	130					135					140				
Leu	Trp	Val	Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	Arg	Ala	Met
145					150					155					160
Ala	Ile	Tyr	Lys	Gln	Ser	Gln	His	Met	Thr	Glu	Val	Val	Arg	Arg	Cys
			165						170					175	
Pro	His	His	Glu	Arg	Cys	Ser	Asp	Ser	Asp	Gly	Leu	Ala	Pro	Pro	Gln
			180					185					190		
His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Leu	Arg	Val	Glu	Tyr	Leu	Asp	Asp
	195						200					205			
Arg	Asn	Thr	Phe	Arg	His	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Glu
	210					215					220				
Val	Gly	Ser	Asp	Cys	Thr	Thr	Ile	His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser
225					230					235				240	
Ser	Cys	Met	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr
			245						250					255	
Leu	Glu	Asp	Ser	Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu	Val
			260				265						270		
His	Val	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn
		275					280					285			
Leu	Arg	Lys	Lys	Gly	Glu	Pro	His	His	Glu	Leu	Pro	Pro	Gly	Ser	Thr
	290					295					300				

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
 305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
 325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
 340 345 350

Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His
 355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met
 370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp
 385 390

<210> 26
 <211> 499
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu
 1 5 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro
 20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser
 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln
 50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala
 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His
 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala
 100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu
 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr
 130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro
 145 150 155 160

Ile	Gln	Ile	Lys	Val	Ser	Thr	Pro	Pro	Pro	Pro	Gly	Thr	Ala	Ile	Arg	165	170	175
Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Val	Val	Lys	180	185	190
Arg	Cys	Pro	Asn	His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser	195	200	205
Ala	Pro	Ala	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ser	Gln	210	215	220
Tyr	Val	Asp	Asp	Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr	225	230	235
Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe	245	250	255
Met	Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	260	265	270
Ile	Ile	Ile	Thr	Leu	Glu	Met	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	275	280	285
Ser	Phe	Glu	Gly	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	290	295	300
Asp	Glu	Asp	His	Tyr	Arg	Glu	Gln	Gln	Ala	Leu	Asn	Glu	Ser	Ser	Ala	305	310	315
Lys	Asn	Gly	Ala	Ala	Ser	Lys	Arg	Ala	Phe	Lys	Gln	Ser	Pro	Pro	Ala	325	330	335
Val	Pro	Ala	Leu	Gly	Ala	Gly	Val	Lys	Lys	Arg	Arg	His	Gly	Asp	Glu	340	345	350
Asp	Thr	Tyr	Tyr	Leu	Gln	Val	Arg	Gly	Arg	Glu	Asn	Phe	Glu	Ile	Leu	355	360	365
Met	Lys	Leu	Lys	Glu	Ser	Leu	Glu	Leu	Met	Glu	Leu	Val	Pro	Gln	Pro	370	375	380
Leu	Val	Asp	Ser	Tyr	Arg	Gln	Gln	Gln	Gln	Leu	Leu	Gln	Arg	Pro	Ser	385	390	395
His	Leu	Gln	Pro	Pro	Ser	Tyr	Gly	Pro	Val	Leu	Ser	Pro	Met	Asn	Lys	405	410	415
Val	His	Gly	Gly	Met	Asn	Lys	Leu	Pro	Ser	Val	Asn	Gln	Leu	Val	Gly	420	425	430
Gln	Pro	Pro	Pro	His	Ser	Ser	Ala	Ala	Thr	Pro	Asn	Leu	Gly	Pro	Val	435	440	445
Gly	Pro	Gly	Met	Leu	Asn	Asn	His	Gly	His	Ala	Val	Pro	Ala	Asn	Gly	450	455	460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His
 465 470 475 480

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr
 485 490 495

Trp Gly Pro

<210> 27

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<220>

<221> modified_base

<222> (15)

<223> inosine

<400> 27

ggcctcgagt acaantwcat gtgtaayag

29

<210> 28

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 28

ggcatcgatt ctcttcagg gcaagcaca

29

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 29

ggcatcgatg aactcacggc tcagctc

27

<210> 30

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 30

tttagtgagg gttaataagc ggccgcgtcg tgactgggag cgc

43

<210> 31

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 31

gccctggagg cggccgctta ttaaccctca c

31

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 32

ggcatcgatg tagacaggca tggcacg

27

<210> 33

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 33

gggctcgagc tgaagaagct gtactgc

27

<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 34
 gggatcgatc tccgtttctt gatggaa 27

<210> 35
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 35
 cctgcctgga cttgcctgg 19

<210> 36
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 36
 ccaggcaagt ccaggcagg 19

<210> 37
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 37
 gaacatgtcc caacatgttg 20

<210> 38
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 38
 caacatgttg ggacatgttc 20

<210> 39

<211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 39
 ccttaatgga ctttaatgg

19

<210> 40
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 40
 ccattaaagt ccattaagg

19

<210> 41
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 41
 atgtcccaga gccacacag

19

<210> 42
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 primer

<400> 42
 agctcatggt tggggcac

18

<210> 43
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 43
cagactcaat ttagtgag 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 44
agctcatggt tggggcac 18

<210> 45
<211> 120
<212> PRT
<213> Murine sp.

<400> 45
Met Asn Phe Glu Thr Ser Arg Cys Ala Thr Leu Gln Tyr Cys Pro Asp
1 5 10 15
Pro Tyr Ile Gln Arg Phe Ile Glu Thr Pro Ala His Phe Ser Trp Lys
20 25 30
Glu Ser Tyr Tyr Arg Ser Ala Met Ser Gln Ser Thr Gln Thr Ser Glu
35 40 45
Phe Leu Ser Pro Glu Val Phe Gln His Ile Trp Asp Phe Leu Glu Gln
50 55 60
Pro Ile Cys Ser Val Gln Pro Ile Glu Leu Asn Phe Val Asp Glu Pro
65 70 75 80
Ser Glu Asn Gly Ala Thr Asn Lys Ile Glu Ile Ser Met Asp Cys Ile
85 90 95
Arg Met Gln Asp Ser Asp Leu Ser Asp Pro Met Trp Pro Gln Tyr Thr
100 105 110
Asn Leu Gly Leu Leu Asn Ser Met
115 120

<210> 46
<211> 81
<212> PRT
<213> Homo sapiens

<400> 46

Met Ser Gln Ser Thr Gln Thr Asn Glu Phe Leu Ser Pro Glu Val Phe
 1 5 10 15

Gln His Ile Trp Asp Phe Leu Glu Gln Pro Ile Cys Ser Val Gln Pro
 20 25 30

Ile Asp Leu Asn Phe Val Asp Glu Pro Ser Glu Asp Gly Ala Thr Asn
 35 40 45

Lys Ile Glu Ile Ser Met Asp Cys Ile Arg Met Gln Asp Ser Asp Leu
 50 55 60

Ser Asp Pro Met Trp Pro Gln Tyr Thr Asn Leu Gly Leu Leu Asn Ser
 65 70 75 80

Met

<210> 47

<211> 26

<212> PRT

<213> Homo sapiens

<400> 47

Met Leu Tyr Leu Glu Asn Asn Ala Gln Thr Gln Phe Ser Glu Pro Gln
 1 5 10 15

Tyr Thr Asn Leu Gly Leu Leu Asn Ser Met
 20 25

<210> 48

<211> 245

<212> PRT

<213> Homo sapiens

<400> 48

Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr
 1 5 10 15

Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn
 20 25 30

Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn
 35 40 45

Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met
 50 55 60

Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp
 65 70 75 80

Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met
 85 90 95

Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys
 100 105 110

Ser Ile Val Ser Phe Leu Ala Arg Leu Gly Cys Ser Ser Cys Leu Asp
 115 120 125
 Tyr Phe Thr Thr Gln Gly Leu Thr Thr Ile Tyr Gln Ile Glu His Tyr
 130 135 140
 Ser Met Asp Asp Leu Ala Ser Leu Lys Ile Pro Glu Gln Phe Arg His
 145 150 155 160
 Ala Ile Trp Lys Gly Ile Leu Asp His Arg Gln Leu His Glu Phe Ser
 165 170 175
 Ser Pro Ser His Leu Leu Arg Thr Pro Ser Ser Ala Ser Thr Val Ser
 180 185 190
 Val Gly Ser Ser Glu Thr Arg Gly Glu Arg Val Ile Asp Ala Val Arg
 195 200 205
 Phe Thr Leu Arg Gln Thr Ile Ser Phe Pro Pro Arg Asp Glu Trp Asn
 210 215 220
 Asp Phe Asn Phe Asp Met Asp Ala Arg Arg Asn Lys Gln Gln Arg Ile
 225 230 235 240
 Lys Glu Glu Gly Glu
 245

<210> 49
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 49
 Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys Gln Thr
 1 5 10 15
 Ser Ile Gln Ser Pro Ser Ser Tyr Gly Asn Ser Ser Pro Pro Leu Asn
 20 25 30
 Lys Met Asn Ser Met Asn Lys Leu Pro Ser Val Ser Gln Leu Ile Asn
 35 40 45
 Pro Gln Gln Arg Asn Ala Leu Thr Pro Thr Thr Ile Pro Asp Gly Met
 50 55 60
 Gly Ala Asn Ile Pro Met Met Gly Thr His Met Pro Met Ala Gly Asp
 65 70 75 80
 Met Asn Gly Leu Ser Pro Thr Gln Ala Leu Pro Pro Pro Leu Ser Met
 85 90 95
 Pro Ser Thr Ser His Cys Thr Pro Pro Pro Pro Tyr Pro Thr Asp Cys
 100 105 110

Ser Ile Val Arg Ile Trp Gln Val
 115 120

<210> 50
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 50
 Arg Gln Gln Gln Gln Gln Gln His Gln His Leu Leu Gln Lys His Leu
 1 5 10 15

Leu Ser Ala Cys Phe Arg Asn Glu Leu Val Glu Pro Arg Arg Glu Thr
 20 25 30

Pro Lys Gln Ser Asp Val Phe Phe Arg His Ser Lys Pro Pro Asn Arg
 35 40 45

Ser Val Tyr Pro
 50

<210> 51
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 51
 atgccagag cacacag 17

<210> 52
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 52
 tccaccaccc tgttgctgta g 21

<210> 53
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 53
gaccacagtc catgacatca ct